

MTIP in the proteomic quantification of network signaling pathway activation in the context of phenotypic heterogeneity. Phospho-expression profiles derived from MTIP analysis may be correlated or compared with genomic and other biomarker information. In the context of PI3K signaling, several single agents targeting the PI3K pathway are under development and in various phases of clinical development (Hassan et al 2013; Fruman and Rommel Nat. Rev Drug Disc 2014). The foregoing results indicate that MTIP can identify patient specific phosphoexpression signatures that may impact personalized therapeutic decisions for inhibiting PI3K pathway activation. The future of successful targeted therapeutics, however, may rely on the use of pathway-specific inhibitors in various combinations (AL-Lazikani Nature Biotech 2012; Bozik et al 2013). In the context of multi-pathway phosphoexpression profiles (e.g. PI3K and MAPK as described in this work), MTIP can provide phospho-proteomic data that can contextualize the use of combination therapies on a per patient basis.

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